

EXHIBIT E

IMMUNOREACTIVE SCORE OF EAG1 EXPRESSION IN NORMAL AND NEOPLASTIC TISSUES						
NORMAL TISSUE (N) ^a			NEOPLASTIC TISSUE (N) ^a			
		EAG1 EXPRESSION			EAG1 EXPRESSION	
		RANGE OF SI ^b	RANGE OF SA	MAX. IRS	RANGE	IRS ≥
Esophagus (4)		0-1	0-3	4	Esophagus carcinoma (8)	5-6 100
Stomach (3)	-surface epithelium and neck cells	0-1	0-2	3	Gastric carcinoma (10)	2-6 89
	-gastric gland parietal cells	1	2-3	4		
	-gastric gland chief cells	2-3	3	6		
Duodenum (2)		0	0	0		
Small intestine		0	0	0		
Large intestine, appendix (4)		0-1	0-3	4	Colon carcinoma (8)	4-6 75
Salivary gland (1)		0	0	0		
Liver (2)		0	0	0	Hepatocellular carcinoma (10)	5-6 100
Gallbladder and bile duct (4)		0	0	0	Gallbladder carcinoma (5)	2-6 80
Pancreas (2)	-ducts	0		0	Pancreatic carcinoma (8)	4-6 73
	-acini	2	3	3		
	-endocrine islets	1	3	4		
Kidney (3)	-tubular epithelium	1	3	4	Renal cell carcinoma (9)	5-6 100
	-collecting duct epithelium	1	3	4		
Transitional epithelium of the urinary tract (5)		0	0	0	Transitional cell carcinoma (9)	4-6 89
Prostate (3)	-glands	0-2	0-1	3	Prostate carcinoma (56)	4-6 98
	-stroma	0-1	0-1	2		
Seminal vesicles (2)		0-1	0-1	2		
Testis (1)	-cells of spermatogenesis	2	3	5		
	-Sertoli cells	0	0	0		
	-Leydig cells	1	3	4		
Cervix uteri (2)	-ectocervix	0-1	0-2	3	Cervical carcinoma (9)	4-6 78
	-endocervix	1-2	2-3	5		
Endometrium (5)	-epithelium	2	2-3	3	Endometrial carcinoma (10)	5-6 100
	-stroma	0	0	0		
Myometrium (2)		0-1	0-3	4		
Fallopian tube (4)		0-1	0-3	4		
Ovary (3)	-surface epithelium	0	0	0	Cystadenocarcinoma of the ovary (10)	5-6 100
	-follicular epithelium	0-1	0-3	4		
	-stroma cells	0	0	0		
Placenta	-trophoblast cells	3	3	3		
	-stroma	0	0	0		
	-Hofbauer cells	1	2	2		
Mammary gland (3)	-ductulo-lobular epithelium	1	3	3	Breast carcinoma (60)	3-6 93
	-extralobular duct epithelium	0	0	0		
Lung (3)	-alveolar surface	1	2	2	Bronchus carcinoma (10)	4-6 90
	-bronchus epithelia	0	0	0		
	-submucous glands	1	2	3		
Lymph node, tonsil, spleen (4)	-surface squamous epithelium	0	0	0		
	-follicle center lymphocytes	0-1	0-1	2		
	-plasma cells	1-2	2-3	5		
	-lymphocytes of the interfollicular area	0	0	0		
	-macrophages	2	3	5		
Thymus (2)	-lymphocytes	0-1	0-2	3		
	-epithelia	0-1	0-2	3		
Bone marrow (1)	-erythropoiesis	0	0	0		
	-myelopoiesis	1	3	4		
	-thrombopoiesis	1	1	2		
Thyroid gland (1)		0	0	0	Thyroid papillary carcinoma (9)	5-6 100
Parathyroid gland (1)		1	3	4		
Hypophysis (2)	-adenohypophysis	2	3	5		
	-neurohypophysis	0	0	0		
Adrenal gland, cortex (3)		1-2	1-3	5		
Autonomous nervous system	-ganglion cells (4)	1-2	3	5		

	-adrenal gland, medulla	2	3	5		
Endocrine pancreas (2)		1	3	4		
Skin (7)		0	0	0	Basalioma, sp/nalloma (10)	0-5 10
	- melanocytes	0	0	0	Malignant melanoma (39)	0-6 37
	- skin adnexes	1	3	4		
Skeletal muscle (3)		0-1	0-2	3		
Heart muscle (5)		0-2	0-2	4		

^aThe number of analyzed cases is shown in brackets;

^bExpression of EAG1 in normal tissue: range of signal intensity, SI; range of positive organ specific cells, staining amount, SA; highest immunoreactive score in the analyzed cases, max. IRS;

^cExpression of EAG1 in neoplastic tissue: Range; range of IRS detected, %; percentage of cases with an IRS \geq .